

MCBV SCAST blasso scalar Ferminding Results - 950472HZ01R Nethodal Bross Results Sold and Resulted (Sign of above to save your search strategy)

### Job Title: Ich8914 (16 letters)

A THE SECT (BENEVES WERE STREET) SHIPS FOR MICE SPECIAL SECTION

Please, by our new design!

## BLASTN 2.2.164

Nationance Stophan F. Altschul, Thomas L. Medden, Xlejendro A. Scheffer, Singhul Sheng, Sheng Kheng, Wabo Miller, and David C. Lipsan 1997), "Ougped BLAST and PST-BLAST: a new generation of proteen database seaton programs," Nocleic Note Res. 25:3389-3487.

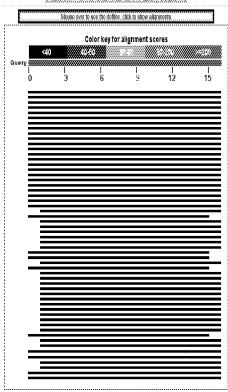
KID: 80047262018

Database: All Gendark HonGu/DDG/49D8 sequences (but no 881, 878, GCS,environmental ramples or phase 0, 1 or 2 MTGC sequences) 7,349,565 sequences; 24,756,383,437 total letters

If you have any gradiens on questions with the results of this search please refer to the  $\underline{\rm NASO}(2NN)$  TaxonNetLEMPORTS

Querya Length-16

# Distribution of 159 Blast Hits on the Query Sequence



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Degend for links to other resources: 🛍 UniGene 🛍 GRO 🚨 Sene 🛍 Skrubture 🚨 Mag Viewer

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	Section 2						
AG186973.20	Clear's handlatin directions 5, done 55 24255, complete executions	22.2	32.2	105%	5.9	105%	
80022285.3	Franciscopiates BAD disco Distri-Modifie from theoreticans it, compute sequences	22.2	32.2	100%	4.9	108%	
No. 117370.3	Symphocoes Unberna arctime-rica healty proach (AT-6575570) (mTMA), comaletie ods	35.2	32.2	103%	9.9	1088	133. <b>X</b> G
ACCOSTO	System a sealine 1940 atoms 1944 atom 1944 of this from 11, compute sequence	92.2	32.2	100%	9.9	100%	
AY150923.1	Mass consculus 2 olego menante treprima adMa. Michael full-longità continha il library: clores della sottanzi library: clores della sottanzi library: clores della sottanzi library: clores della sottanzi continha il library:	52.2	32.2	100%	9.9	105%	<b>31</b> 3
F7128283.1	for existing policy that down a Play 15-60 (FRZUZ_ 5-20 m) RRUA, complete using	32.2	32.2	105%	9.9	105%	200
X0980121.1	Onus rouseable States mean on extrain a cell CIG. 2008 SPR-4997 (2014), RIMEN Inchrogate encloded library, dance SPR-1957(SPS and duct, enclosed library dance). It is extrained to the support of the su	22.2	32.2	166%	9.9	100%	(3) (4)
APS02215.1	Skryas solite (species authres-gross) genote DBA, decentres s	32.2	272	100%	8.9	100%	
AL596327.5	Systems DDA eleganos from dozie 99 F-1 9254 is a dhromiseanie 5, comulato eleganos	82.2	32.2	1035	0.9	1088	
A0178926.1	Practivings codigo or PRA for DNA polytomase alpha adulytic visionity, gardal cos	52.2	32.2	100%	9.9	100%	88

A0020018.2	System on spiles stranspormer 15 diatro (FIT) 552505, composite sequences  Amenificació desdense 700 de composite sequences  Amenificació desdense 700 de composite sequences No. 5 de	22.2	32.2	169%	5.9	100%	
M.186545.2 M.086715.1	Quandidopsis ricidane ETAX di ricinazione di, config fragmant No. 44  Varialidopsis ricidane UTAX di ricinazione di, PAXC di ricinazione di PAXC di Ricinazione	32.2	02.2	100%	8.9	100%	65
14012055014	White rousealles servines are 15, servine 825 53855, confider experies	32.2	32.2 32.2	100% 100%	9.9	100%	<b>8</b>
PANGGARA	Spycochiacytalo se, POD 8830 TANA, Campleto genome	52.2	112	105%	9.9	100%	
X15500.3	Special colored (2, 55.2), 2010, 816.3, Same Start (1945.)	22.2	32.2	166%	9.9	100%	
87904525.1	Analidopos circitare Anaptisei (F-2011), 2001, proc., complie a circ	22.2	32.2	100%	8.9	100%	<i>33</i>
AP0034SE 5	Compas asilins Jaconics Group genomic Data, donor seasons 6, PAC stone Palestal II.  Voryes asilins Jaconics Group genomic Data, donor seasons 6, PAC since Palestal II.  Voryes asilins Jaconics Group genomic Data, donor seasons 6, PAC since Palestal III.	32.2	32.2	100%	9.9	100%	
<u>AF005420.3</u> (GF000018.1	Continuents Sportine area of the Continuents of the Continuent of the Continuents of the	92.2	32.2	100%	9.9	100%	
5882049.1	Magality parasitate Full warph (UNA Conspiral sequence from circle CSS 1799: 1797 of Founty's and builts of attain only or Alabotopus tealine (from press)	22.2	32.2	100%	9.9 8.9	100%	O.E
(X15472.1	Egypachwynydd g fir gana far gynarwa transgontar	22.2	22.2	100%	8.9	100%	
VALSCERY( 8	Stower CMA adoptions from others (1923-3515 AP or on unposoner 2 Container that 2" and or a round goes, a risectional ancient 20st (APICE) (AP	82.2	32.2	100%	0.9	108%	
466 (0020000608.)	\$0mmganda yasuulae 65 noole (Ozarki Kill (1485), m 1884	85.2	36.2	93%	39	100%	Œ
050000567.1	Magapharona esterificilis relial. 5., conspliate genome	20.2	56.5	53%	38	100%	
36/192938.1	Charler ratio at una 21 - 12-70 fa S. n. 1940 (dulika source 1950). 19-95 (1950), comprehe usa	20.2	30.2	92%	30	105%	<b>MO</b>
\$0x62918.1	Deallor ratio all control 4-54-10.8, million (Stiffs double MOX 154-144-144 MAX 25-031749), comprete add	20.2	30.2	92%	39	100%	() <b>T</b>
fospatary.	Professional priorit Sharary, compiled a genome	20.2	56.5	95%	39	100%	
(6000081.1	Auditive Rollin (1715 1994), complete speniore	80.8	36.2	93%	39	100%	
\$46 001302593.5	Charge makey: Total in byrosica ligrae Annie protein pactial in PRA	30.2	30.2	93%	38	100%	
078.001867124.1	Azematic bilator Statisti Have Importantian protein pr	30.2	30.2	93%	38	100%	<u> </u>
[288_001889500.0	Consider Statos SPARS HBB NAD distinguis distinguis portas partis in HAR.  Louiser a bilator SPARS HBB NAD distinguis distinguis del private partis in HAR.  Louiser a bilator SPARS HBB NAD distinguis del private partis in HAR.	52.2	30.2	93%	39	105%	<u> </u>
XM_001577512.0	Vinearish autori accomme mass per sem organism entre organism conservation of the cons	20.0	30.2	92%	30	100%	0
XM, 001776865.1	Symptomic following proteins produced group per extramates Symptomic following proteins produced group (SYMPNORM) (145195) mRMA, pentilel odo	20.2 20.2	30.2	93%	39 39	100%	<u>0</u>
602110973	Solvanii (pagassiano dirantesame 5 close Cili69:m512821, conqliete explante	30.2	30.2	93%	39	100%	. M
ACCOUNTS A	Sisting series BAG comes CRDS+118F+7 from subrome even-es, complete ecopy-ance	5775 2674	30.2	93%	39	100%	
2015959868112	Costroller DNA sequence from stone CNSEP - 2855 in Schwyg grow; 3. complete sequence	32.2	30.2	92%	39	100%	
C25:00005.1	Residence separation (DW 100+), comparts genome	20.2	20.2	99%	29	100%	
300,551104965.5	Special visits of colors of states of the st	30.2	30.2	93%	39	108%	376
80188931.12	Sone fracious: June 77: 201521, samples sources	89.2	36.2	93%	39	100%	
01575204.8	Selandia: DNK assumes from stone DNEY-P22.2 in indiagn group 14, complete sequences	30.2	30.2	93%	38	100%	
MONROONEA	of an implicate a PAST done is OPAST - AND OF INTERFED as a sequence as a composite analysis as a sequence as	20.2	30.2	92%	39	100%	
29100205.1	Sasticación readori PETS, completo geranno	39.2	30.2	99%	39	100%	
M153244.2	Office windfare, notific (NEXIX) of 100, who he genome - during or servicence	55.5	36.2	93%	39	100%	
1994_nationseed	Sweldebyels the Same In port in dease 2 solution is leading ground (ATCS 15050) million, complete adds	X1.2	30.2	93%	38	100%	(3E)
136156948.1	(Danierania al 2011-27 et 5.5, in 99 vii (d) Nik done (MACE 27 55 et 6), garrial cols	32.2	30.2	92%	39	105%	( <b>)</b>
2M.768889.1	Copylosocos nesionnesis ves. nodicini ene S-500 M hypothetica gruten TCHSICSTRI partie in RNA	20.0	30.2	93%	39	105%	0
becomments	(Carlo Francisco control despose Augusta (Carlo) - Aces, complete sequences - View in confidence Sent Chican - Deletic mon decomence at commission equences	20.2	30.2	93%	39	100%	
80105866.4 Enggesta a	Painting polyres and a service of the accommendation of the accomm	80.2 se s	30.2	95%	35	100%	
AG155003.2 AG15533.3	Ornescolla nellacoperir disconsuma CP, compicte acquierca	20.2	56.5 351	100%	39	100%	252
G2500801.1	Shrakanate ripplings ve hi NAS 400, monites genans	30.2 30.2	92.9	92%	39	100%	Œ
07020255.15	Statematics DEM appropriate internal done CP-211-175809 to littin says group 15, comprised expresses	30.2	59.5	93%	39	100%	
85214869.4	Consequela realizaçatar oranosamo (C. considela septembra	80.2	248	102%	39	100%	83
BEQUARKEE	(Consignal or animosal or animosal of compute secuence	89.2	351	100%	38	100%	8
AG197081.2	Plant traglodyles SAD Idans CR281 SEX.13 from chromosomo 7, concelleiro associanos	30.2	30.2	93%	38	100%	
AMagasza 1	velocolectes econogross ur. Onesite complete genome, et rein in service frames	20.2	56.5	92%	39	100%	
29300249.1	Printicobades cycles MPRIX: completels genome	30.2	56.5	95%	39	100%	
DANGALI	Melekaprila gelaspeace DV415 paramic segui acca	2012	36.2	93%	39	100%	
000000001	Suchlistics Stations of the GNTT221 ACQ 1990 (report in both 2 science from youther (ACQ 1990) on PRA, complete als	SAZ.	30.2	93%	38	100%	136
100_122265.1 Feb. 22226.2	Similations trademic insportin better 2 submoit family ground (APTS) (2555) in RNA complete acts  Virallineary transcrive areas mittir (4414), complete sequence	32.2	30.2	92%	39	100%	M.M.
MO188200.20 Incoverse s	Considerations reactor action libra ACP-see (CTNTT) prices, control calcium.	30.2	30.2	93%	39	100%	
(Marsona.) (A0139500.)	Mula masalla 900 tong 900 story in thom story care is a sequence.  Mula masalla 900 tong 900 story in thom story course is, complete sequence.	30.2	3.00	95%	39 90	100%	
AU190221.12	(Musi naturallus dinnovements, danne 1929-272117, complein seguente	90.2 30.2	30.2 30.2	93%	39	100%	
MO1010201.15	Vinia russalins streament is, dans 4703 11190, complete sequence	20.2	30.2	93%	39	100%	
800033523	Violes coupoulies 9AG vione 9592-924KS from internessonie 18. complete soquence	30.2	30.2	95%	39	100%	
A0185381.6	Part traplogres SAO doos 59-4-160.16 it to a discoverage 7, complete septemb	99.2	30.2	93%	38	100%	
A0166538.4	Onus muerallus chromesmen 5, dans 9724-20476, considere sequinnes	20.0	30.2	93%	39	105%	
AC104255.2	Virills troubulits SAC don't 5924-542Ns from attendisonal init, particular sequences	20.2	30.2	93%	09	100%	
80028175.5	Male rouseables service OSTGLiab du randorme à dans RECO-05 NSC, completa expenses	89.2	30.2	93%	39	100%	
AG125542.52	Majo masalino deconserva 17, dona 1925-2111-1 , complexe approace	50.2	30.2	93%	38	100%	
AG126438.2	films rousellus BAC sonn RP2-4-2KLTs from shrin sessore 10, complete sequence Vision rousellus 9AD done RP2-4-2KLTs from shrin sessore 12, complete sequence	30.0	30.2	93%	39	100%	
80133493.5 80115080.52	Value rouseulus conne marson etim o connecutation in cultimine sequences  (Mus musculus connecutation on the PSE > 1/2/1000, complete sequences	30.2	30.2	93%	09 9e	100%	
A011808012 A0188218.2	Musicusculus deconcernor URF data 922-27.15, complete sequence	99.3 99.3	36.2 56.5	96%	39	100%	
M0000000	drawno seglers Paol store 1994 Asia Ela riam 1, completa asquarces	20.2	30.2	92%	39	100%	
18.021725.2	Grownon DDA sequences from done 994-826762 on characteristic Supplies 1, 21,2 Contains thin 2 and in the 1990's given for integral remaining problem on problem and a kinesia family consider 45 (KFHS) gaussing processing according according according to	30.2	30.2	93%	35	100%	Œ
4.003384.20	When the december from the PCT 1-559/16 in the consistence of Contains the Contains	35.2	30.2	95%	39	100%	. 60
A0205552.3	Curability sets the harm in the monoscore of charge CT.5.4.4.4 maps or 1000, comprete secuence	\$775	30.2	93%	38	100%	<b>3</b>
AGM55GLA	Surabiosysis challens thromocome 2, dann FT58AS insprinting, complex sequence	20.2	30.2	93%	38	100%	23
A0680238.2	Channel septims X and 1971-605-W (Reams) Park Claricer Investigate Hornes and Ulbrany), comprete sequence	20.2	30.2	93%	39	100%	
08718854.6	Tatración riginarios N.D. Hergis : 2004	20.2	20.2	93%	29	100%	
25703816.2	Tetraceon igramida full-length (ENA	35.2	30.2	95%	35	100%	
1	Corpus sating ((species millions group) generals DNA, decreases a	30.2	58.5	93%	38	100%	
#20525A.1.		0	1			1	
#505216.1 6856136.1	Debaryone pees herseall disconsense F of state. 1997-F of Debaryone remeable	20.2	56.5	92%	39	100%	
#90521A.1.	Observances reseall divoraceurs if of state 000927 of Ordervances transactive of the conditive space of the condition of t	0	i :	92% 95%	39 39	100% 100%	

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AS/008188.4	(Overeitha nelanogerier, anomorna 25, injuni 5662-5651), BAC done SACKSSTS. Cominies requires	22.2	30.2	93%	39	105%	
A0004015.6	France spales SAD core SP 1-497 france, complete beginning	20.2	56.5	93%	39	100%	1
82003451.3	Organ zelles Jezonice Greco gerannic DNA, decompanne E. PAC score Piloti EGI7	80.2	36.2	93%	39	102%	
B3866238.0	(Paut traplicly) es droma aoma 22 claire 1779 in 1611 i 27, mag 22, complete acquisitions	32.2	30.2	93%	38	105%	1
285/00103-1	from trapplacines commonstrate 20 elinis PTB-117811, mea 20, parties sequencies, comprete securence	20.2	30.2	93%	39	100%	
66/04/88/8	Corps ealins describe Group geoons DNA shromsomer B. 64C done CUITE 1.764	30.2	30.2	93%	09	100%	1
80,598220.1	Citypiocococa neodicinaria near, seediran ana sicilar hippotherical circlem (CIOLS 4672) year oli nin Mis	80.8	36.2	93%	35	102%	() <b>T</b>
07992550.)	Claudia gendus frontend claude. Conne Crestiffica agrica	20.5	36.2	93%	39	102%	20
AR015288.1	(Blacework) anxistemia Mirt, complete gename	52.2	105	93%	38	105%	-
MONSHABA.	VALIS TOUSDUMS (NAC DODGE FOR LATUR TOUR TAIL SUMPACE SEQUENCE	20.2	30.2	92%	39	100%	

Alignments

	Pan troglocytes coromosoma 22 clone: PTB 117K17, med 22, pertier sequencia, comprete sequence
186908 186 B	Cryso estina Japonios Croup genomio DNA, chromosomo B, GAC clone: Cut 21 _ H54
860,599323.1	Organicoccus meetermans van involormans JEC21 hypothetical cretein (CNLS 4570) partial miRNA
05092550.)	Sissive gavius thrushad vCNA, done Ch69F116g23
A:015250.1	Shawaneta meidensia M5-1, ormplete genoma
A0154438.2	Okils musculiks BAC coma RP24-140E82 from 14, complete sequence
Get selec	sted sequences
: Deliacios	277.701 🏙 Canis familiacis chromosome 9, clone XI-24085, complets segmence
Lengte=19476; Score = 32.; Edenticies : Strand=Plus	2 bits (16),   Expect = 9.9 = 18/56 (1028), Gage = 0/16 (0%)
Query 1	CONTINUARCORANCA 16 ETHERITERS 6 STSTEARSFORMER 101901
	255.5 M Par trogledytes BMC close CRIST-496614 from chromosomo 7, complete
requence Geograph-16985)	4
Strand=Plus.	
	GTGTCMAAGCCRAACA. 16   EE   EE   EE   EE   EE   EE   EE   E
>□ milMil mRNA, compis Length~2309	1992.1: (NEW Acapidopsis theliana proline-rich family protein (4740195%)) to cit
	TAS ATAMISM ( profine-rich family protein (Arabidopsis theliens)
Identifies : Strand-Flus.	2 bits (16), Bopes = 9.9 = 16/15 (100%), Gops = 9/15 (0%) /Flos
Duery I Sbjot 2098	CTGTCGARGCCGARGA 16 CTGTTGTGTGT GTGTGARGCGARGG 2111
Gength=12116	
Score = 31.1 Identifies : Strand-Flus,	2 bits (16), Expect = 9.9 = 16/15 (100%), Gaps = 9/15 (02) /Flos
Query 1 Shjet 72053	GTGTCAAAGTCAAACA 16 HEHEHEHEHEH GTGTCAAAGTCAAACA 19866
	3268.21 XXE Hus mosculus 3 days magnate thypos coma, NINEA full-length encional metabliculus procust unclassifiacia, full mosc
GEL:GELDXGE	205. Name : transforming growth factor bate regulated game 3 5] (10 or Kower Publish Elaka)
	2 bits (i6), Espect = 9.9 = 16/16 (1004), Saps = 0/16 (0%) Micros
	GESTOARACKORACK 16 ELECTRICIETE GESTOARACKORACK 1865
>□gbiASi28i Length=S134	285.11 XXII Arabudopsis thaliana AT4g18540/725412_220 MRMD, complete ode
CONF. 201. 2C	ISSE AIGUSTES   prolime-mich family grotain [Amabidopsis thaliana]
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-	GTETPAMICENARCA 18 THETPAMICENARCA 1936
	elicitic (CCCC) Mor resculus bone varnow strona cell CC2-2018 SR-4907 CCR2, ECCCN enciched library, clone:041071623 productionclassifiable.
toil-length ( full insert :	
toll-length ( full insert ) Length=2526 (MSIK.IDE.20	
tull-length of full insert : Length-2920 - GMNE ID: 20 [Mis misculu: Score = 32.]	paquanca <u>VN. Nord:</u> i transforming growth factor bata regulated game 3 8) (19 <b>or favor Nobba lixic</b> ) 2) data (18), Ingent = 3,5 = 16/16 (1093), Rogs = 0/18 (US)

> 🗖 (021168/0821221) 🏙 Oryta sativa (japonica cultivar-group) genomic DDA, chromosome o Lengto÷30731885

> Sort alignments for this subject sequence by: E value Sonce Patrage relateity Quary stary position Suggest start quality.

Eastures Flanking Whis part of subject sequence: 23926\_mo.st.St.suder\_6x85g8816986 4256\_mo.st.D.suder\_6x85g816986

Scors = 32.3 bits (16), Expect = 9.9 Identities = 10/16 (100%), Gaps = 0/18 (0%) Strand=Plus/Miles

STGTCMARGCCMARCA 15 Sbjer 6093485 GTGTCAAAGCTAAACA 6093470

Peatures flanking this part of subject sequence. 25491 be ac 51 side: 030600575400 42850 op at 3: aide: 1880A-58 ricosconal 60%

Score = 30.2 bits (15), Expect = 39 identifies = 15/15 (1008), Sags = 0/15 (0%) Strend=Plus/Plus

Query 2 IGOCARAGCCARACA 15 

Peacures flanking this part of subject sequence-16464 by at 5% 51664 029560726709 20352 by ac 3% stdet 039860307500

Score = 28.2 hits (13), Espect = -613 Hdentifies = 13/13 (100%), Gaps = 0/13 (0%) Strand=Plus/Plus

Query 4 TCAMAGCCAMACM 16 

Features flanking this part of subject sequence: 57781. op. at. 31. ander. 080590353900 15581. bg. at. 31. sldst. 080590754500

Score = 26.3 bits (13), Expect = 612 Identifies = 13/13 (100%), Gaps = 9/13 (0%) Strend-Flas/Minas

 Query
 4
 TORRAGONARDA 16

 Sbycc
 14330334
 TORRAGONARDA 14330322

Deatures in this part of subject sequence:

STCARASCORARC 15 

Peatures flanking this part of subject sequence: 1876.pp.ab.13.stder.0808n0853806 478.pp.ab.21.stder.0808n0853000

Score = 26.3 bits (13), Espect = 612 Identities = 15/15 (100%), Gaps = 9/13 (0%) Strand=Plus/Minus

GTCAAA99CGAAAC LS 

Factures in this part of subject sequence: 05669521500

Score = 28.3 bits (13), Expect = 612 identifies = 13/13 (1008), Sags = 0/13 (08) Strend-Plus/Minus

Query 3 STORRAGOCRARO 15 Sbjet 24001305 GTCAAAGCTAAAC 24001293

Peatures flanking this part of subject sequence: 11585 bp. at. 57 sida: 250/g0/27702 117135 bp. at. 57 sida: 1808-455 ribosomal SNA

Score = 26.3 bits (13), Emped. = 612 Edentifies = 13/13 (100%), Gaps = 9/13 (0%) Strand=Pins/Mions

 Query
 4
 DOMAGNOMANCA
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 Sbjet
 24976660
 ICMAGNOMANCA
 24976688

Features flanking this part of subject sequence: 2015/2021 at 2: 2006. Seb5@828:00 1925/2021 at 3: 3:562.0295@8688:0

Score = 26.3 bits (13), Expect = -612 Identities = 15/15 (100%), Gaps = -9/13 (0%) Strend=Flus/Flus

Query 4 TCRAAGCCRARCA 16 

Deatures in this part of subject sequence:

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Score \sim 26.3 bats (13), Expect \sim -612 Identities \sim 15/15 (100%), Gaps \sim -9/13 (08) Strend-Flus/Minus
                   TGTCARAGCCRAA 14
Query 2
> anti(A1505227.5) W Human OWA sequence from clone RA11-116F24 on chromosome 1, completa
sequence
Isoquin=94737
 Scora = 32.2 bits (16), Expect = 9.5 Identities = 16/16 (100%), Gaps = 0/16 (0%) Scrand-Plus/Mines

        Quarry
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pactial eds
Longth-4692
Score = 32.2 bits (16), Expect = 2.9 Identifies = 16/16 (1608), Saps = 0/16 (0%) Strand=Plus/Plus
Query 1 SIGTCAAMSCCAAACA 16
Ships 224 GREENAAGCCAAACA 239
 > □gb/ACC2215.4: 30 domo sapiens corposome 19 clone CID-325229, completa sequence
 Score = 32.2 bits (18), Expect = 3.9 
Edenticias = 16/16 (1808), Saps = 0/16 (0%) 
Strand=Plus/Plus
Query 1
                 CTGTCAAAGCGAAACA 16
Shigh 100469 GTGTONAAGCCAAACA 100464
Describilists Continues (M) Arabidopsis thalana (M4 coronsserve 4, continues tragment No. 40
 Score = 12.2 bits (18), Expect = 9.9 identifies = 16/16 (10%), Gaps = 9/16 (0%) Strand=Plus/Plus
> Revolation continue with Arabidopsis thatiase OVA chromosoms 4, RAC clone (2801) (CSSAI)
project)
Length-110102
 Score = 31.2 bits (16), Expect = 9.9
Edentifies = 16/15 (180%), Gaps = 9/15 (9%)
Strand=Flus/Flus
Query L GTGTTAAAGCTAAACA L6
> 🗖 <u>(b)AC) 25683.431</u> 💹 Mus amsomlus chromosoma 15, clone 8P25-253920, complete sequence
%ength-175021
 Score = 32.2 bits (36), Expect = 9.8 Edentitios = 16/15 (IRGE), Gaps = 9/15 (98) Strend-Plus/Plus
Query I GTGTCAAAGCCAAACA 16
Sbjet 86913 GTGTCHAAGCCAAACA 86926
> 🗖 <u>(10)1820/00072.31</u> 💹 Symeobodystis sp. PCC 6803 DMR, complete genome
                                                                         fort alignments for this subject sequence ov:
                                                                          č value Siore Renoent Loentity
Guere stant position Subject stant position
 Peacures in this part of subject secuence:
   salanesyl ditnespect of surject
glanesy thenepoot protein
 Score = 32.2 bits (18), Expect = 9.9 Mentirias = 16/16 (10%), Gaps = 0/16 (0%) Strend=Plus/Plus
                  GTGTCAARGCCAAACA 16
Shiet SAU0513 SIGTERAAGCCAAACA SA00526
 Features in this part of subject sequence:
   solenacyi diphosphane synchase
 GYGICARAGCCARA LA
01101101101010
Sbjct 2077:48 SIGTCAAASCCAAA 2077161
Factures in this part of subject sequence: selected, diphosphate synthese prinsermal profess. R
 Scors = 25.3 bits (13), Export = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
StrendeRius/Minus
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        Query
        4
        TCSANGCCAARCA
        16

        Sbyck
        2100610
        TCXAAGCCAARCA
        2100604

 Pastures in this part of subject sequence:
schemesch.niphochlets.apurmase
sensory nearablemion histibine himase
  Score = 26.3 bits (13), Expect = -6.2 Identities = 19/13 (100%), Sage = 0/13 (0%) Strand=Flus/Minus
                            TCAMAGCCAMACA 15
> and NISSAS JINYSKAR Symethocystis PCC 6903 gloP game and OSP2
  Scora = 32.3 bits (15), Expect = 9.5 Identities = 16/18 (100%), Seps = 0/18 (0%) Scrand-Plus/Dines
Quary 1 GOGICAAAGCCMAACA 16
Sbjer 194 SIGYCAAAGCCAAACA 178
 > anistossilli XXX Arebidopsis thaliana 214q19560/F28012_220 gene, complete cds
  6884 Co. $2556 AT4618570 | proline-rich family protein [Arabidopsis thaliana]
  Score = 32.2 bits (15), Export = 9.5 Identities = 16/15 (100%), Gaps = 0/15 (0%) Strand-Flus/Flus
Quary 1 STGTCAAAGCCAAACA 15
Sbjer 1675 GTSICANAKKCAAACA 1890
 > 🗖 <u>doji62003408.31</u> 🌺 dryta sativa Vaponica Group genomic DWA, onrovosowa 6, FBC clone:E0436011
Length=169550
  Scors = 32.2 bits (16), Expect = 9.5 Identities = 16/18 (180%), Gaps = 9/18 (0%) Strand-Paos/Minos
Quary 1 STGTCAMAGCCAMACA 15
(Highlighthi)
Sbjer 7504 GTEICANAGCCANACA 7289
> \square \frac{d_{111162035425,11}}{d_{11162035425,11}} \stackrel{6}{\bowtie} orçue setiva Vaponica Group genanco DRA, chromasoma 8, FAC olona:F0544802 Length-144954
  Scors = 32.3 bits (16), Expect = 9.5 Identities = 16/16 (100%), Gays = 0/16 (08) Strand=Flus/Minus
Quary 1 GISICWAMSCOMAMIA 16
> 🗖 <u>guil0203000,11</u> 🕷 Candidates Blockmannie pennsylvanious str. SPEM. complete genome
Length=791654
 Features in this part of subject sequence:
  Score = 32.2 bits (18), Expect = 9.9
Edentities = 16/16 (180%), Sags = 0/16 (0%)
Strand=Plus/Plus
                              GUGUCAAAGCCAAACA 1.6
 > 🛮 <u>ominiPXXXAAN, NYXXXAAN</u> XXXXX Arabidopsis thaliana Full-length cDMA Complete sequence from
cione SSCTMERTEF15 of Liowers and buds of scrain coi-O of Arabidopsis
theliana (thuis occas)
Length-2022
  Score = 32.2 bits (26), Expect = 9.8
Edentities = 16/25 (180%), Gaps = 9/16 (0%)
Strand=Plus/Plus
Query I STSTCAMAGCCAMACA 16
SUBJECT 1937 GTGTCAMAGCCAMACA 1952
> \square antichargain \square Symechocyclic gir gama for glucose transporter Length-1559
  SERNING MARKET | glucose transport protein [Symechocystus sp. BCC 8803]
 (10 or faver PubMed Ilaka)
  Scors = 32.2 bits (16), Expect = 9.9
Identities = 16/18 (100%), Gaps = 0/18 (0%)
Strand-Plus/Minus
Querry I GOGTONAAGCONAACA 18
HITHERITETTE
Sbjet 155 GIGTCAAAGCCAAAA 180
> Description of the second general process representation of the content of the 
  Score = 32.2 bits (16), Expect = 9.5 Identities = 16/16 (100k), Gaps = 0/16 (0%) Strand=Glos/Minos
```

Share 30100 crompayornayary 30105 > <u>racing 00009809.11</u> **B** Decemphila yakuba GE16496 (Dyak\GE16496), MENN GENE ID: 8523573 DychigE16496 | GE16496 gens product from transcript GN16496-8A [Drosophila | jakuna] (10 or famer Publish Links) Score = 20.2 bits (15), Espect = 39 Edentifies = 15/15 (100%), Gaps = 0/15 (0%) Strand=Plus/Plus > □gb/CCOUNATAL: ∭ Mycopleasma arturitidis 15813-1, complete genome Length=820453 Sont alignments for this subject sequence by: E value Score Rescent identity Seconstant position Società stant position Deatures in this part of subject sequence: exodsoxyriixoneslease v. aigba sidunit Score = 20.2 bits (55), Empset = 39 Identarias = 15/15 (100%), Gaps = 0/15 (0%) Strand=Plus/Minus SISTCAAMSCUAAAS 15 Peatures in this part of subject sequence: conserved byporberical protein Scors = 25.3 bits (13), Expect = 61.2 Identities = 13/13 (100%), Gaps = 0/13 (0%) Scrand=Flus/Dinos Quary 2 ISICA4ASCCAAA 14 0500 684186 TOTCAA60CAAA 684174 > anisotististiii 🕮 Danio rerio sitchill-67e18.9, MRGA (CDMA chone MYC:194306 IMAGC:9037290), complete ods Length+3303 SERG ID: 382721 sira211-67418.3 : sirch211-67418.9 (Danio reruo) (19 or fewer Probled Links) Score = 30.2 bits (L5), Espect = 39 Mentriles = 15/15 (100%), Gaps = 0/15 (0%) Strend=Plus/Minus SUBSTITUTE STATE S > DabbC182818.1: XXI Danio rerio si.ch211-67e16.9, mPNA (MDNA clone MGC.194349 IMAGE:9637292), complate ods Length+3303 SECR. 10: 538763 siteh271-53e(f.\$ ) stich211-67e16.9 (Danie verie) (10 er force PubMed Minks) Score = 30.3 bits (15), Expect = 30 Identities = 15/15 (100%), Gags = 0/15 (0%) Strand=Edus/binos Quarry 2 DGTCMAAGCCMAACA 16 Sbjer 2650 IGTCAAAGCCAAACN 2465 > 🗖 <u>quicrolo72.22</u> 💥 Helioobacter pylori Shi470, complete genome Length=1698548 Sort alignments for this subject sequence by: E velue Romas Percent identitus Gerg arang position Subject start position Features in this part of subject sequence: oligoshdopeptidass F. cpepfl Scora = 30.2 bits (15), Expect = 39 Identities = 15/15 (100%), Gaps = 0/15 (0%) Scrand=0lus/0lus ISICAAASCCAAACA 16 Peakures in this part of subject segmence: hypotherical protein Score = 26.3 bits (L3), Expect = -612 Identities = -13/13 (100%), Gaps = -9/13 (0%) Strand=Plas/Plus TUARAGOURARCA 16 Sbjet 1475300 TOARAGCCAARCA 1275312 > 🗖 <u>dbilAPDV7281.11</u> 💥 Lactobacillus reuteni F275 DMA, complete ganome Length=2033414

Scors = 30.2 bits (15), Expect = 39 Identities = 15/15 (100%), Gaps = 0/15 (0%) Strand=Elus/Flus Quarry 2 TOTORANGCORARGA 16 http://blast.ncbi.nlm.nih.gov/Blast.egi.(7 of 20)8/27/2008 3:54:42 FM

Peatures in this part of subject sequence: dell stage deservities and six first

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> Distribute 10 to the proper malaya Turnilin-tyrosine ligase family protein partial
mRMA
Lengte=2086
  GRAN, Co. 8128133 Red (5685) | Tubulin-tyrosine ligase family protein
 [Brugia malegi] (16 or fewer FubMed links)
  Score = 20.2 bits (15), Espect = 39
Edentifies = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Degri (2015) 1915 (1915) 🚨 Laccaria disolor 2030 4881 hypothetical protein partial 2008
CONG. TO: AMERICA LACATIONNET LINES; | hypothetical protein [taccaria hicotom $2358-827] (id or fower Publish Nicks)
 Score = 30.2 bits (15), Empact = 39
Edentrios = 15/15 (100%), Gays = 0/15 (0%)
Strend=Plus/Plus
Query 1 TGTCBAAGGCBAAGA 16
Sbjot 300 ISTCA4ASCCA4ACA 3).4
mRNA
Length=1669
GENERAL 10: 5081238 LANGILBANT 392305 | NAD-Alconydo dehydrogonase
[Laccarta bicolor 52389-682] (10 or fever Problec Links)
  Score = 50.2 bits (15), Expect = 38 Identities = 15/15 (100%), Gaps = 0/15 (0%) Strand=Fins/Minos
Query 1 STGTCAAAGCCAAAC 15
> 1/25/18/9 00/2775/2013 1 Laccaria bicolor 3239N-892 NAD-dependent aldehydo dehydrogenaso
pactial oRMA
Length=1425
SENC JO: 8070831 LACGIONACT 188093 | MAD-dependent alcomyde dehydrogonase [Baccacia Micolon 8298M-M80] (10 cr fower Publied Links)
  Query 1 GDSICARAGCCARAC 15
 > Droffty 001784205 [] 💆 Phaeosphaeria moderum SNIS hypothetroal protein partial mRMA
  SENE TO: 5571016 SECO.COTOM : hypothecidal protain [Phasosphasria modocum SW15]
  Score = 20.2 bits (15), Espect = 39
Mdentities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 7 TGTCAAAGCCAAACA 16
 Sbjot 906 ISTCHARGOCKARCA 592
 > modification of the physical patent of the property of the p
mRNA, partial cds
Length=1311
2008 ID: 538931 PRYPROMENT 143838 | appothetical protein
[Physicaniticalla gatone subsp. gatone] (10 or dower Publical links)
  Score = 30.3 bits (15), Expect = 39 Identities = 15/15 (100k), Expe = 10/15 (08) Strand=Flus/Minus
Quarry 1 GOGICAAAGCCAAAC 15
Ships: 488 GIGTCAAAGCAAAC 474
> Doga NCC 11085 At M Solarum Tycopersicum chromosome 6 clone 00851m0132E21, complete
sequence
Nangto=136760
  Score = 30.2 bits (15), Expect = 39 Edenticies = 15/15 (100%), Eags = 0/15 (0%) Strand=Plus/Minus

        Quary
        2
        TETCARAGCCARACA
        18

        sbjet
        21302
        TGTCARAGCCARACA
        21289

  : 🗆 <u>alikulinne.n) 🎘</u> Gailus gallus dad olone 04261-13917 froe obrososome s, complete
 sequence
Longth=S11741
  Score = 30.2 bits (15), Espect = 39 
 Edentities = 15/15 (100%), Gaps = 0/15 (0%) 
 Strand=Plus/Plus
Query 2 IGTCAAAGCCAAACA 16
 Sbjet S132 DGICAAAGCDAAACA B156
```

> Deablings:5582.121 WW Sebratish DNA sequence from clone ONEX-13M23 in linkage group

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Scora = 30.2 bits (15), Expect = 30 Identities = 15/15 (100%), Gaps = 0/15 (0%) Scrand=Flus/Flus
 Quary 2 ISICA4ASCCA5ACA 16
Shjet 154250 TGTCAAGCCAAGCA 154264
 > and one of the state of the s
   Features in this part of subject sequence:
         translation indication factor 19-3
  Score = 30.2 bits (15), Expect = 38
Edentifies = 15/15 (1008), Saps = 0/15 (0%)
Strand=Plus/Plus
                                               TSTORANGOCRANON 16
 SUMMER STATES OF STATES OF
   : 🗖 <u>cedime 20110/818.11</u> 🎎 denio recio sitchili-57el6.8 (sitch2l1-67el5.9), mama
   objection 100 Danio ratio stico211-67e16 9, NAME (come clone w901031767 IMAGEN:8027509),
    SEME 10: 558102 situabil-65816.8 ( sitch211-67016.9 (Danio cenio)
  (10 oz favez PubNed Ilaka)
   Score \approx 39.2 bits (15), Expect \approx -39 Identities \approx 15/15 (100%), Gaps \approx 9/15 (0%) Strend-Flas/Minus
 Query 1 TGTCAAAGCCAAAGA 18
 Sbjet 1095 TGTCAAMGCCAAMCA 1081
 > Digital 1888 20 131 MM damis familiaris, close XX-237824, complete sequence
   Score \approx 39.2 bits (15), Expect \approx -39 Identities = 15/15 (180%), Gays = 9/15 (0%) Strend-Flus/Flus

        Query
        2
        TGTCKAAGCCAAACA
        16

        Sbjet
        50911
        TGTCKAAGCCAAACA
        50825

  > 🗖 <u>authicT513284.6)</u> 🕷 debcefish DWA sequence from clone OXE1-26203 in linkage group
 14. complete sequence
Languh:150961
   Scora = 30.2 bits (15), Expect = 39 Identities = 15/13 (100%), Gaps = 0/15 (0%) Scrand=Plus/Ditos
 Quary 2 TGTCARAGCCARACA 18
 Shiet 84950 DGICAAACCAAACA 84030
  >□<u>qhiAcivi372.31</u> ∰ Pan thoglodytes BAC clone CH251-56696 from obromowome x, complete
 sequence
Length-170491
   Score = 30.2 bits (15), Expect = 39 Mdentixias = 15/35 (1008), Saps = 0/45 (0%) Strand=Plus/Minus
 Query 2 TGTCAAAGCCAAACA 16
  Peatures in this part of subject sequence:
   Score = 30.2 bits (15), Empset = 39
Identifies = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
                                           TGTCAAAGCCAAACA 16
  > \square and 1000372(94.6) 88 Yetus winefers coming WTPX103020.19, whole games shorton, sequence Langtin-0456
   Score = 30.2 bits (15), Espect = -39 Identities = 15/15 (100%), Gaps = 0/15 (0%) Strand=Plus/Minus
 Query 1 IGTCAAAGCCA4AC4 16
  > Decimal 001093336.1; WWW Arabidogsis Chalcana importion beta-2 subunit family protein ($12016980)
 mRNA, complete ods
Length-1518
   9808,201,918189,073616360 \pm exportin beta-2 subunit family protein
 [Acabidopsis thaliana]
   Score = 50.2 bits (15), Expect = 39 Identities = 15/15 (100%), Gaps = 0/15 (0%) Strand-Plus/binos
 Quary 2 ISTCAAASCCAAACA 16
 Shier 507 TOTORANGCRARGE 400
```

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>□ghikuliskauli XXI danio rario sich211-67e16.9, maxa (cDMA clone IMAGE:8759845),
partial ods
Length-1965
    2208 ID: 538302 sitem211-63a(6.8 : stich211-67a)6.8 (Danio merio)
 (10 or fawer PubMed 11nks)
  Score = 30.2 bits (15), Except = 39 Identities = 15/15 (100%), Gaps = 9/15 (9%) Strand=Plus/Wites
Quarry 2 ISTCAMAGGCAMAGA 16
Shjer 760 TGTCAAAGCCAAACA 746
 > 1:81.86.28620.11 Cryptococcus neoforwars ver. neoformens 8-3501A hypothatical
protein (CMBI2270) partial ASRA
Langua = 1545
  GNAL IL: 9938167 (NOISI70 | hypothesical protain
 [Cryptococcus meeformans var. neeformans 8-3501A]
  Score = 30.2 bits (15), Expect = 30 Mdenticias = 15/15 (160%), Sages = 0/15 (0%) Strand-Plus/Plus

        Onerry
        1
        GTSIGNAGCCANAC
        15

        Ebjot
        1526
        STGTCAAGCCAAAC
        1540

  ⊃ □<u>gb/ACG6425.///</u> 🌺 Cenis familiaris chromosome 2+, clone XX-1414, complete sequence
 Length-163090
  Score = 10.2 bits (15), Expect = 39 Mdenticiae = 15/15 (1008), Gaps = 0/15 (0%) Strand=Plue/Minus
Query 2 TOTOANAGCONNACA 16
 Tellellellellelle
Sbjot 97967 TGTCAAAGCCAAACA 47953
  🗦 🗖 <u>g&180125555.4. 🏶</u> Gen troglodytes BBC clore CR251-359N21 from chromosome x, complete
 zequence
Wength-157737
  Score = 30.2 bits (55), Empect = 39 
 Tdentriiss = 15/15 (100%), Gaps = 0/15 (0%) 
 Strend=Plus/Plus
Query 1 TGICAAACCCAAACA 16
 Shigh SEGOT TEXTRAAGCCAAACA 68821
> Interpretation of the standard of the control of 
 sequence
Length-167001
                                                                                                                          Sort alignments for this subject sequence by:
                                                                                                                               t value Scors Percent Loanting
Westy start position Subject start position
  Score = 30.2 bats (15), Expect = 39 Identities = 15/15 (100%), Gaps = 9/15 (08) Strand-Flus/Binus
 Score = 25.3 bits (13), Expect = -6.2 Identifies = 12/13 (100%), Saps = 0/13 (0%) Strand-Plus/Plus
Quary 1 GYGTCAAAGGCAA 13
Length = 211.46705
                                                                                                                          Sort alignments for this subject sequence by:
                                                                                                                                E value Sonce Perseon identity
                                                                                                                              Owery start position Suggest start question
  features flanking this part of subject sequence:
      13070 no st 51 cmlet 0315115-84
1704 no st 10. stdet 0315115-84
  Score \sim 30.2 bats (15), Exgect \sim -39 Identities = 15/15 (100%), Seps = (/15 (0%) Strand=Flus/Flus
                                   TGTCARAGCCRAACA 16
Features Flanking this part of subject sequence.
$645 No. 20.51 side: 001515-85, icoform 8
1831 No. 20.51 side: 0036016-85
  Score = 28.2 bits (14), Expect = 155
Edentities = 14/14 (1508), Sags = 0/14 (5%)
Strand+Pius/Plus
Query 1 SIGTCAAAGCCAAA 14
Features in this part of subject sequence:
      032030-92
  Score = 29.2 bits (14), Expect = 155 Identities = 14/14 (180%), Gaps = 9/14 (08) Strend-Flus/Flus
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Shiet 11067757 TGTCARAGCCRAAC 11087770

Features in this part of subject segmence: CG1A371-PA

Score  $\approx$  29.2 bits (14), Expect  $\approx$  155 identities  $\approx$  14/15 (180%), Gaps  $\approx$  9/14 (0%) Strand-Flus/Mines

 Querry
 1
 GEGETRALAGECTARA
 14

 Sbjet
 15077405
 SEGTRARAGECTARA
 19077392

Destures in this part of suggest sequence: 001887FEB

Score = 26.2 bits (13), Espect = 613 identifies = 13/13 (160%), Saps = 0/13 (0%) Strand=Pits/Minus

 Quary
 2
 TSTCAAASCCAAA
 14

 sbjet
 1654155
 DGTCAAAGCCAAA
 1854163

Psetures flanking this part of subject sequence: 20067 by at 5% sides 0012894-089 landoms B 2015 by at 5% sides 000282-08

Score = 26.3 bits (13), Expect = 612 Identifies = 15/15 (100%), Gaps = 9/13 (0%) Strend=Flus/Mirus

Query 2 TGTCAAGGCCAAA 14
|| | | | | | | | | | | | | | | | | |
| Shyct 8618064 TGTCAAGGCCAAA 6818052

Faatures in this part of subject saquence: 288529-86. isoform 5

Score = 26.3 bits (13), Expect = 612 identicias = 13/13 (1008), Saps = 0/13 (0%) Strand-Plus/Minus

Omery 4 TCAAAGCCAAACA 16 111111111111 25jut 8231937 TCAAAGCCAAACA 8821925

Peatures in this part of subject sequence: CGP187-PR, Lintons R CGP187-PR, lintons R

Score = 26.3 bits (L3), Especi = -612 Edentries = -13/13 (10%), Gays = -9/13 (0%) Strend=Plus/Plus

 Ownery
 3
 STCAARSCCAAS
 15

 Sbjct
 11416000
 GTCAARSCCAAC
 11416020

Features in this part of subject sequence: 005784-86, icoloru.B COCCSA-9A...Workers.A

Score  $\sim 26.3$  bits (13), Expect  $\sim -612$  Identities  $\sim 15/15$  (100%), Gaps  $\sim -9/13$  (08) Strand-Flus/Minos

 Quency
 S
 GTCMARGCCRARC
 15

 Slight
 18757753
 STCAAASCCAAAC
 18757741

Features Flanking this part of subject sequence. 2020 to ac.5% side: GS2015-26% assistant & 20502.pp.st.3% side: GS2020-26

Scors = 25.3 bits (15), Expect = -61.2 Edenticies = 19/12 (1908), Exps = -9/13 (0%) Strand-Plus/Minus

 Quacty
 2
 IGMCAAAGCCAAA
 14

 Sbjot
 14477073
 MGICAAAGCCAAA
 14477061

Peatures in this part of subject sequence: LSITS21-PA

Score = 26.3 bits (E3), Expect = -612 Identities = 15/15 (100%), Gaps = -9/13 (0%) Strend-Flus/Minus

Peatures in this part of subject sequence: 0017884-94. Rendern A 0017884-90. Listing G

Score = 16.3 bits (15), Expect = -612 Identities = 19/13 (100%), Gags = 9/13 (0%) Scrand=Flus/Flus

 Querry
 9
 ICMANSCRAMACA
 16

 Sbjet
 16324541
 TCMANGCRAMACA
 16324553

Peakures in this part of subject segmence: CSLSSOS:RA

Score = 26.3 bats (E3), Expect = 612 Edentities = 15/13 (100%), Gaps = 9/13 (0%) Strand=Plus/Plus

  $> \square_{ab}$  (COMPANAL)  $\ggg$  (Shawarelle fragidinarane WCIMS 400, complete general Language 404227

Sort alignments for this subject sequence by: E value Secre Researt Resulty. Cose: stact counties Collect Stack position

Destures in this part of suggest sequence: Sic pricein/Metal

Score = 20.2 bits (13), Espect = 35 Edentities = 15/15 (100%), Saps = 0/15 (0%) Strand=Plus/Plus

 Query
 2
 ISTCAAASCCAAAAA
 26

 0101010101010101
 0010AAACCAAACA
 3204525

Features in this part of subject sequence: inthisoming aidoless

Scora = 25.3 bits (13), Expect = -61.2 Identities = 19/13 (100%), Gags = -0/13 (0%) Scrand=Flus/Flus

Features in this part of subject segmences axion acid cacrier protein

Score = 26.3 bats (13), Expect = 612 Identifies = 15/15 (100%), Gaps = 9/13 (0%) Strand=Plus/Plus

Overy 4 ICAPACCCARACA 16
Sbyct 3483427 TCARAGCCARACA 3263439

Sort alignments for this subject sequence by: I value foots Percentifications Very stark position Subject start communic

Score  $\sim$  39.2 bits (15), Except  $\sim$  39 identities  $\sim$  15/15 (100%), Gaps  $\sim$  9/15 (0%) Strend-Flus/Minus

 Querry
 2
 TGTCAPAGCCAPACA
 16

 Sbjet
 30345
 TGTCAPAGCCAPACA
 50328

Score = 28.2 bits (14), Expect = -156 Edentities = 14/14 (1608), Saos = 0/14 (09) Strand-Plus/Minus

Quary 3 GTCAAMSCCAAACA 16 HITTERSTEEL 17167 GTCAAAGCCAAACA 17167

: Da<u>kiakulikki, ki</u> Www Drosuphila malanogastar dhrosusema 31, cumpleta sequence

Sort adigments for this subject sequence by: E value <u>Sence Patheon identity</u> descriptant position Subject stact position

Eastures flanking this part of subject sequence: 12124 no.at.5: ards: KSE2221-6A 20184 No.at.5: adds: KSE521-6A

Score = 39.2 bits (15), Expect = 39 Identities = 15/15 (100%), Gaps = 0/15 (0%) Strand-Flos/Winos

Peatures in this part of subject sequence: C115755-68

Score = 28.2 bits (54), Espect = 155 Edentities  $\sim 14/14$  (100%), Gaps = 9/14 (0%) Strand+Plus/Mions

Query 1 GOGGAAGGCAAA 14 13113113111111 Sbact 3817898 GIGGGAAGGCAAA 3817585

Esatures flanking this part of subject sequence: AAAA to at 11 side: CREADA-FA 1881.no.at.11 side: CREADA-FA. Asoform.A

Score  $\sim 29.2$  bits (14), Expect  $\sim -155$  Identities = 14/15 (100%), Gaps = 0/14 (08) Strand-Flus/Plus

Quarry 2 TGTONAGGORAAC 15
([1][[1][[1][[1]]]
Sbjet 679490 TGTCANAGCRANC 679493

Teatures floaking this part of subject sequence: 128 no.et 5% order CGISSIN-RA 889 No.et 3% aloes CGSSESERRA

Score = 19.2 bits (14), Expect = 155 identities = 13/12 (100%), Gaps = 0/14 (0%) Strand=Plus/Plus

 Querry
 3
 GTCSAAGCCAASCA
 16

 sbjet
 17420295
 GTCAAAGCCAASCA
 17420308

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Features in this part of subject sequence:
 Score = 28.2 bits (16), Expect = 155 Identities = 14/12 (100%), Gags = 0/18 (0%) Strand=Phas/Plus
                      GTOMARGOCARACA 16
Peatures flambing this part of subject sequence.
Inde by at 51 size. CORRELES.
11983 by at 51 size. CORRELES. Issteam &
 Score = 28.3 bits (13), Expect = 612 identifies = 13/33 (1003), Saps = 0/(3) (08) Strand-Plus/Plus
Query 1 GIGTCAAAGCCAA 13
Sbjot 6792359 SIGTCAAAGCCAA 6792371
Score = 26.3 bits (13), Espect = 612
Edentifies = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Mious
Query 4 ICANACKCANACA 16
0([0][0][0]])
Sbyot 8801511 TCAAAGCCAAACA 6801489
Features in this part of subject sequence: ONLYARI-PA. ListSon.A
   QQUISRI-PB/...180face..6
 Score = 26.3 bits (13), Expect = -612 Identities = 15/15 (100%), Gaps = -9/13 (0%) Strend-Flas/Minus
Quary 9
                     TORRAGOCORRAGA 16
Deatures in this part of subject sequence:
   0013138-88
0032158-88
 Scors = 25.3 bits (13), Expect = -612 Identities = 19/13 (100%), Seps = -0/13 (0%) Strand=Fluc/Ninus
> □<u>qtiaggi4287.21</u> ‱ ūrosophila melanogaster dhromosoma 3R, complete sequence
Lenoub - 27905053
                                                                           Sort alignments for this subject sequence by:

2 value | Scool | Parcent Mandrid

| Mesty state Lossinian | Support Interference
 Features flanking this part of subject sequence: 13545 pp. et. 3: ander CC13645-84
    30563 bp. at. 31 siles: 0003649-94
 Score \approx 30.2 bits (15), Expect \approx -39 Identities \approx 15/15 (100%), Gaps \approx -9/15 (0%) Strand-Plus/Wines
                     TGTCARAGCCRAACA 16
Sbjet 20904520 TGTCAAAGCCAAACA 2050A506
Teatures in this part of subject sequence: CT4681-98. Aschorn 8
XX4881-88. Liantern 8
 Score = 28.2 bits (14), Expect = .155 Identities = .12/12 (100%), Gaps = .0/14 (0%) Strand=Flos/bitos
Query 1 SIGTCAAASCCAAA 14
Peatures in this part of subject segmence: (SANIX-PA
 Score = 20.2 bits (14), Expect = 155 fdentities = 14/14 (1008), Gaps = 9/14 (08) Strend=Plus/Plus
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GTGTCAAAGCCAAA 14 Sbjcc 12147722 STGTCAPAGCCAPA 11147785 Factures in this part of subject sequence: CTALLS-RC. Profess C Score = 28.2 bits (14), Expect = 155 Mdentirias = 14/14 (1008), Saps = 0/14 (0%) Strand=Plus/Plus Query 3 STCAAASCCAAACA 15 Sbjet 11255312 GTONAGGCOARACA 11235325 Peatures flanking this part of subject sequence 1959 bt at SI sees OCCOVIDE 1 2000 ENGLISH NO. 1200 Peat N. 1200 Peak N. 1

Score = 26.3 bits (13), Empet = 612

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TGTCARAGCCARA 14
Features flanking this part of subject sequence.
$201.bp.at.$1.adem.001288:00
id10.bp.at.$1.adem.001888-92
 Score = 28.3 bits (13), Expect = 612 identificts = 13/13 (1008), Saps = 0/(3) (08) Strand-Plus/Plus
                  TORNAGCORARDA 18
Operv 3
Ebjet 3039033 TCNAAGCCAAACA 3039045
 Peatures in this part of subject sequence: CGRANTLERA
 Scors = 25.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Mitos
Quary 1 STGTCNANGCCAA 1S
Sbjet 3675741 GTGTCAAAGCCAA 5875728
 Peatures in this part of subject sequence: CD288-88
 Score = 26.3 bits (13), Espect = 613
Edentities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plos
Query 1 STGTCNAAGCCAA 15
Eastures flanking this part of subject sequence:
1000; pp. at 2: side: 010122-64
2791 bp. at 3: side: 0133235-64
 Score \sim 26.3 bits (13), Expect \sim 612 Identities \sim 15/15 (100%), Gaps \sim 9/13 (0%) Strend-Flas/Minus

        Query
        1
        стегоздаесска
        13

        Slijek
        19652752
        стегоздаесска
        19652760

 Deatures in this part of suggest sequence: 005405-FC. Incform C. 005405-FE. Laufoum B.
 Score = 25.5 bits (15), Expect = 61.2 adentities = 19/13 (190%), Gaps = 9/13 (0%) Schand=Flus/Flus
Quary 5 GROANAGOONANG 15
SEJET 19830127 STCAAAGCCAAAC 19830139
 Peakures flanking this part of subject sequence.
12116 bp.ar.S. side: 0551652-P2
34068.rp.at.11.arde: C616816-PA
 Score = 26.3 bits (13), Expect = 612 Edenticias = 13/13 (1008), Gaps = 0/13 (0%)
  Strand-Plus/Plus
Query 2 TGFCAAAGCCAAA 14
 Peatures flambing this part of subject sequence doll not at all sides, CC34834-848
ADRE Do at all sides, CC34834-848
 Score = 26.3 bits (13), Espect = 612 fdentities = 13/13 (100%), Gaps = 0/13 (0%) Strend=Flus/Minus
Query 4
                     TORRAGOORANCA L6
 Features in this part of subject sequence: 0031090-974, 1301000-9
    CG21000-Pty. isoface.t
 Score ~ 26.3 bits (13), Expect ~ 612 Identities = 13/13 (100%), Gaps = 9/13 (0%) Strand=Dias/Flus
                      TORMASCORARCA 16
 > Doguđa<u>2183821.N1</u> WW Mar trogladytes BAC clone CD251-202133 from chromosoma 7, complete
sequence
Languh = 157744
 Score = 30.2 bits (15), Expect = 30
Edentities = 15/15 (180%), Sags = 0/15 (0%)
Strand=Plus/Plus
Quary 2 ISICA4ASCCAAACA 16
Shjet 103631 TOTCAAAGCCAAACA 103645
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>  $\square$  applications of the strain strains of the strain strain strain should be strain sh

Cont alignments for this subject sequence by:

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Features in this part of subject sequence:
  Scors = 39.2 bits (15), Export = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Stread=Flos/Winos
Querry 2 TOTCAAAGCCAAAGA 16
Sbjor 953182 TGTCAAAGCCAAACA 953168
 Pastures in this part of surject sequence: conserved importatioal process with anidebysiclase deach.
  Score = 26.3 bits (13), Empact = 612 filentifies = 13/13 (100%), Gaps = 9/13 (0%) Strand-Plus/Plus

        Query
        4
        ICAMACCCAAACA
        16

        sbydt
        1517629
        TCAAAGCCAAACA
        1517641

> \square_{10010100021111} ) delicoracter pylori BFSG1, complete genome Dength-1596366
                                                                                                                                             sons alignments for this subject sequence by:
                                                                                                                                              E value Score Seresut identity
Tuesna start position Subject start position
 Peakures in this part of subject segmence: oxigosodopsetidate.I
  Score = 30.2 bits (15), Espect = 35
Edentities > 15/15 (160%), Saps = 9/15 (0%)
Strend=Flus/Flus
 Features in this part of subject sequence: hepathetical protein
  Score = 28.3 bits (13), Expect = 612 Identities = 13/13 (1008), Sags = 0/13 (0%) Strand=Pius/Minus
Query 0 TORAGGCAGAGA 18
: \square_{\underline{chi00134134.11}} Meleagets gallopavo 07491 ganomic saquanca
Lengto=1050
  Score = 30.2 bits (15), Expect = 38 Edentities = 15/15 (100%), Sages = 0/15 (0%) Strand-Plue/Minus
Query 1 GTGTCAAAGCCAAAC 15
 SEGET 604 GIGTONARGONARG 590
  : 🗖 <u>ellopantius 11.</u> XXXII Arabidopsis thallana clone pENIX221-At2g16560 importio bera-2
- — <u>neuroconternal neuron</u> Arabidopsis thallana clone pE
sucunit family protein (Ar2g16980) mRNA, complete ods
Length=1518
CONG. Not. 80:198 AICS18860 ( importin beta-2 submnit family protein [Prabidopsis thaliana]
  Score = 30.2 bits (15), Expect = 39 Elemities = 15/15 (100%), Gaps = 9/15 (0%) Strend-Plas/Mions
Query 2 TOTCHASCCCHASCA 16
Shict 507 TGFCAAAGCCAAACA 490
> Description 12739.11 WARD Archidogolo khalisma importin baca-2 eutomic family protein (ATCGE996) mBMA, occupante cus
Languarde 1646
\underline{\rm GRME}(DC,S)\underline{\rm MARS}(MMSG) is possible beta-S subunit family protein [Arabidopsis challeng]
  Score = 30.2 bits (15), Expect = 39 Edentities = 15/35 (160%), Eags = 0/15 (0%) Strand=Plus/Minus
Query 2 ISTCA4AGCCA4ACA 18
 Sbjet 456 TSTCAMAGCCAMACM 442
> \square_{QL(201201201301)} Weedinago truncatois oloma util-Seni3, complete sequence Length-19506
  Score = 30.2 bits (15), Expect = 39 Identities = 15/15 \ (150\%), Gags = 0/15 \ (0\%) Strand=Pius/Winus
Quary 2 TGTCAA4GCCAAAGA 18
INTERPOLATION ASSESSMENT TO THE STATE OF THE
 > aghtto2020092.11 Lactobacillus menteri actin-like ATPass (ic1411) gens, partial
eds
Length#343
  Score = 30.2 \text{ hits (15)}, Espect = 39 \text{ Mdentities} = 15/15 \text{ (100%)}, Gaps = 9/15 \text{ (0%)} Strand=Plus/Plus
Query ? TGTUAAAGCUAACA 16
Sbjot 275 ISTCAMASCCMAACA 289
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> Dightatification & Mus musculus BAC clone RF23-167721 from chromosome 16, complete
sequence
Length=211870
Scors = 39.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
                TSTCAMAGCCAMAGA 16
> \square angleCl30281 (3) \cancel{M} Nos musculus chromosome 3, clone RP23-37211), complete sequence
Isagih=215261
Scors = 30.3 bits (15), Expect = 39
Identities = 15/15 (100%), Caps = 0/15 (0%)
Strand=Flos/Winos
Quary 2 ISICAAASCCAAACA 16
> 🗖 <u>aptAC191381 i5;</u> 💹 Mus musculus chromosoma 5, clone R923-119813, complete sequence
Lenotch=209590
 Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Flus/Flus
Quary 2 TGTCAMAGCCAMACA 15
Sbjer 39001 TSICAAACXCAAACA 39005
> Daniaci43492 31 WM Mus nusculus BAC clone RP24-38486 from chromosome 18, complete
sequence
Length=239075
 Scora = 10.2 bits (15), Expect = 39 
 Edenticies = 15/15 /1508), Saps = 0/15 (0%) 
 Strand=Plus/Plus
Query 2 TGTCAAAGCCAARCA 18
: 🗖 <u>alikulasiki.ki</u> 🎉 san troglodytes BAC cione RP43-55016 from chromosome 7, complete
zequende
Length=155929
 Score = 20.2 bits (15), Espect = 35 fdentities ~ 15/15 (100%), Gaps \times 9/15 (0%) Strand=Plus/Micus
Query 1 GTGTCAAAGCCAAAC 15
> 🗖 <u>ublAC164588.41</u> 🕷 Mas musqulus amromosoma 5, alome RP24-304K2. complete sequence
Derigth=188600
 Score = 20.2 bits (15), Espect = 39
Identifies = 15/15 (100%), Gaps = 9/15 (0%)
Strand-Plus/Plus
Query ? TGTCMAAGCCMAMCA 16
Sbjet 109506 ISICAAASCCAAACA 109520
> DataCi68298.2) Mas musculus BAC clore RF24-342R8 from chromosome 16, complete
sequence
Length=206806
 Score \approx 39.2 bits (15), Expect \approx -39 Identities = 15/15 (190%), Gaps = 9/15 (9%) Strend-Flas/Mines
Query 1 TGTCAPAGCCAPACA 16
Shjet 76346 TETCANAGCCANACA 70326
> 🗖 g6/86023/27 4/ 🏁 Mus musculos straio 057866/0 chromuscome 6 clone RP23-25Vil, completa
sequence
Langua = 22,326.6
Score = 50.2 bits (15), Expect = 30 Identities = 15/15 (100%), Gaps = 0/15 (0%) Scrand=Plus/Bitos
Quarry 2 TOTCARAGCIARACA 15
> 🗖 <u>quiloc170548.i51</u> 🕷 Mus musculas chromosomo 17, clone SP23-211H11, complete sequence
Length = 198829
 Score = 30.2 bits (15), Expect = 30
Identifies = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Glos/Winos
Quarry 2 ISICWAAGCCWAAGA 16
> \square <u>aniholitical.51</u> \cancel{M} Was masorius BAC clone K924-243415 from chromosome 10, complete
sequence
Length=160728
Score = 30.2 bits (15), Expect = 39 identifies = 15/15 (100%), Saps = 0/15 (0%) Strand=Plus/Ninus
```

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Share 135633 moreascompason 135696
⇒ □ <u>at 180139452.31</u> ∰ Wite priscaline BAC clone RP23-195KiO from chromosome 19, complete
zequence
Length=218688
 Score = 20.2 hits (i3), Espect = 38 Kdentrites = 18/i5 (100%), Saps = 0/i5 (0%) Strand=Plus/Minus
> Diblacil3935.131 WW Mus musculus chromosome 14, clone R923-312M23, complete sequence
Length=324556
 Score = 20.2 bits (15), Espect = 39

Identifies = 15/15 (100%), Gaps = 0/15 (0%)

Strand=Plus/Minus
Query 2 TGTCNAAGCCNAMCA 16
Sbjet 145583 DOCKAAGCCAAACA 145569
> Data (133210.1) Minus musculus chromosome UNX clone RF23-27012, complete sequence
                                                                                                                                       Sont alignments for this subject sequence by:
 E-value <u>Score Receset identity</u>
                                                                                                                                           Newny stact position. Subject stant position
 Score = 30.2 bits (i5), Expect = 38 % % Rightistas = 15/i5 (1000), Saps = 0/i5 (0%) % Strand-Plus/Plus
Query 2 TOTOANAGCOMMACA 16
Belieffeller S7762 TGTCAAAGCCAAACA 87776
 Score = 26.3 bits (33), Expect = -612 Identities = 15/15 (100%), Gaps = 9/13 (9%) Strend-Flas/Minus
Query 1 TGTCAAAGCCAAA 14
SENSON SE
> 🗖 <u>goracumativ 71</u> 🕷 Hood sapians PAC clone RP4-665C4 from 7, complete sequence
Genoth-105881
 Score = 30.2 bits (15), Expect = -39 Identities = 15/15 (100%), Gaps = 9/15 (0%) Strand-Flas/Plus
Quary 1 TGTCAAAGCCAAACA 16
SEGET STOR TOTOLARGUCALAGE STAR
> autiliaini36.21 www duran DNA sequence from clone RF4-696922 on chromosome Xq21.1-21.2
Contains the 3^{\prime} and of the XIM2A gene for integral mambrane protein 2k and a kinesim facily member 9k (XIFAA) pseudogens.
complete sequence
Length=70665
 Score = 30.2 bits (L5), Espect = -35 Edentities = 15/15 (100%), Gaps = 0/15 (0%) Strend=Plus/Mirus
> 🗆 <u>valialististigg 💥</u> Human DRA requence from clone RP11-553M16 on obromosome 1 Contains
In secondariation of the Bosen DDA requests from clone RPI-583 the 3' end of the gene for a novel protein (PIUI6618), a ribosomal protein 16 (RPIG) pseudopens, the RXVII gene for examinicase b, the 5' end of a ribosomal protein 1673a (RPIG) all pseudopens and a CyG feland, complete sequence length-043667.
 Score = 30.2 bits (15), Expect = 39
Identifies = 15/15 (100%), Gaps = 9/15 (0%)
Strand=Plas/Plus
Query 1 DEIGAPACCHARCA 16
> Dighth 2008/97.20 Mind Acabidopsis thatiana chromosome 2 clone T15J14 map mi398, complete
sequence
Length=114041
 Scors = 39.3 bits (15), Expect = 39 Identities = 15/15 (100%), Gaps = 0/15 (0%) Strand=Flus/Flus
Quarry 2 TGTCAMAGCCAMACA 16
Sbjet 70021 TSICAAACKCAAACA 70035
> Quiaccessic at Americansis thatiana chromosome 2 clone (12824 map mi398, complete
sequence
Langth=93861
 Scora = 30.2 bits (15), Expect = 38

Edentifies = 15/15 (100%), Sags = 0/15 (UK)

Strand=Pius/Minus
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o □ <u>ghiMC245182.71</u> 🌺 domo saplens X 5MC RP11-605.M (Roswall Camb Cancer Institute

 Quary
 2
 TETORAGCOMARCA
 18

 liftHillHill
 18
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 sbjet
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 TGTCAPAGCOMARCA
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Length+54425
 Score = 30.2 bits (15), Expect = -39 identifies = 15/15 (1008), Saps = 0/15 (0%) Strand-Plus/Minus
Query 2 TSTSANAGSSANAGA 18
Ebjet 29782 TGTCAPAGCCAPACA 29768
> 🗖 accitR101884.21(Nt9588) | Tetraceon nigroviridis full-length cDNA
Longth-562
Score = 30.2 bits (15), Expect = 39 Identifies = 15/15 (1608), Saps = \theta/15 (0%) Strand=Plus/Plus
Query 1 SIGTCAAAGCCAAAC 15
Shipet 324 GTGTCAAAGCCAAAC 328
> \square gazzicki095542.2408595882 | letracoon migroviridis full-length cDNA
Length-502
 Score = 30.2 bits (15), Expect = 39 Identizias = 15/15 (1608), Saps = 0/15 (0%) Strand=Plus/Plus
Query 1 SIGTCAAMGCCAAAC 15
Ships S24 GTGTCAAAGCCAAAC S28
 > 🗖 ghill@002014.11 🎇 (nyza satuva (japonica cultivar-group) ganomic 1984, chrovosone
 .
Length=28434780
                                                                 Sons alignments for this subject sequence by:
                                                                   E value Store Remont learnity
Owene start position Subject start position
Feakures flenking this part of subject sequence.
A664 by at Ni aide: DSC940227209
SZVI.by.at.Si.aids.http?c20227409
 Score = 30.2 bits (15), Expect = 39 
Identifies = 15/15 (100%); Gaps = 0/15 (0%) 
Strand-Plue/Plue
Query 2 ISTCARASCCARACA 16
Peatures in this part of subject sequence: 020000454460
 Scors = 39.3 bits (14), Expost = 155 Identities = 14/14 (100%), Gaps = 0/14 (0%) Strand=Dius/Flus
hansenii
Langto=1336804
                                                                 Sort elignments for this subject sequence by:
                                                                   E value <u>Serce Percept Percept</u>

Descriptor, position Societa start position
 Features in this part of subject sequence:
   unasmed protein product.
 Score = 10.2 bits (15), Expect = -35 Wdenthrian = 15/15 (100%), Gaps = 0/15 (0%) Strand-Plus/Plus
Query 2 IGTCNAAGCCGAACA 16
Sbjet S19620 TSTCAAAGCCAAACA S19634
Peatures in this part of subject sequence: Notabad profesio perfect.
 Score = 26.3 bits (13), Expect = -612 Identities = 13/13 (100%), Gaps = -9/13 (0%) Strand=Plus/Flus
               TORGROSSON TA
Quarry 9
Features in this part of subject sequence:
    nepathetical proisin-transmembrans prediction
 Scors + 50.2 bits (15), Expect + 39 Identities > 15/15 (100%), Gaps > 0/15 (0%) Strand=Plus/Minus
Query 2 ISICA4ASCCA4ACA 16
> \square q_{ALMCN,2432,AM} \stackrel{\text{Min}}{M} Non numerous chromosome 5, close LP24-357A23, complete sequence Length-1807D2
 Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gags = 0/15 (0%)
Strand-Pius/Plus
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http://blast.ncbi.nlm.nih.gov/Blast.cgi (18 of 20)8/27/2008 3:54:42 PM

Query 2 TGTCAA4GCCAAAC4 18

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> Duración de Alactonica XII inosophila melanogaster, chromosome 2K, region 5642-5861, RAC
clore RACROSIIS, complete sequence
Length*160650
 Score = 30.2 bits (15), Expect = 39 Edentities = 15/35 (1908), Eags = 0/15 (0%) Strand-Plus/Plus
Quary 2 TGTCAAAGCCAAACA 16
25jet 145636 TOTCHARGUCHARCH 145650
> attacostorous: M Homo saptems RMC clams RP11-49F1 from 4, complete sequence
Lancto=87574
                                                                    Sort elignments for this subject sequence by:
                                                                      E value Sonce Petreon relation
Onervistery position Support start desirion
 Score = 30.2 bits (15), Expect = 39 Identities = 15/15 (100%), Gaps = 0/15 (0%) Strand-Plus/Plus
Quary 2 TGTCAAAGCCAAACA 15
Sbjet 49534 TSICARACCCARACA =0546
Score = 26.2 bits (13), Espect = 612 identities = 13/13 (10%), Gaps = 0/13 (0%) Strend+Plus/Plos
Query 4 TONAAGOONAACA 16
BUILDING TOWARD TRANSPORT
> \square \underline{\text{Mortions}_{AB}(ABL_{GL})} \aleph Dryza sative Jeponica Group genomic DNA, chronosome 9, PMC clone:90812807 Amogit=182546
 Score = 20.2 bits (15), Espect = 39
Edentifies = 15/25 (100%), Gaps = 0/25 (0%)
Strend=Plus/Plus
Query 7 PSICAMACK SMAACA 16
> 🗖 <u>dbjila50/0238.jj 🏙</u> Pam troglodytes chromosome 22 clone:PTE-105%12, map 22, complete
sequences
Length=242704
 Score = 30.2 bits (15), Expect = -39 Identities = 15/15 (100%), Gaps = 9/15 (9%) Strand-Flas/Wines
Query 1 TOTCAAAGUCAAACA 16
SEJECT 100570 TOTCHARGEGRACK 100566
> dojiasaGG132.1: W Pan troquodytas chronosome 22 clone:PIB-417%(), cap 22, pantial
sequences, complete sequence
Length=124900
 Scora = 50.2 bits (15), Expect = 39 Identities = 15/15 (100%), Gaps = 0/15 (0%) Strand-Plus/Flus
Quarry 2 TGTCAMAGCCAMACA 15
> \square <u>durisheddrid3.11</u> \ggg Organ seriva Caponica Group genomic DNA, chronosome 8, BAC clone:001221_B04 Length=12987
 Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (150%), Gaps = 0/15 (0%)
Strand=Flus/Plus
Quary 2 ISICWAMGCSAAMGA 16
> 🗓 <u>xxx1000 [88020.1]</u> XXXX Cryptococcus meoformans was, meoformans JECC1 myorthetical protein
(C4L04576) partial oMAA
Length+1708
SECT. SECTION CONCESSIO | hypothetical protein [Cryphococome montemment work membranes JEC21] (IC or Rever PubMed Links)
 Score = 20.2 bits (15), Empect = 39
Edentities = 15/15 (100%), Gays = 0/15 (0%)
Strand=Plus/Plus
Query 1 GISICANACKONAGE 15
> Dephick187058.11 XX Gallus gallus finished comm, clone ChEST118g23
Longth=1587
 Score = 30.2 bits (15), Espect = 39
Edentries = 15/15 (100%), Gays = 9/15 (0%)
Strand=Plus/Minus
Query ? TGTCMAAGCCMAACA 16
Ships 962 ISTCAAASCCWAACA 648
> \square_{1001332033212} \ggg Shewarelle oneidensis MM-1, complete genome Dongth-9989203
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Sort alignments for this subject sequence by: E-value Score Reposit identity

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features in this part of subject sequence:
        paccetnesata kidase
  Score = 30.2 bits (15), Expect = 38 % % Modernities = 15/35 (1008), Saps = 0/15 (0%) Strand-Plus/Minus
                                      TGTCASAGCCARACA 16
Peatures in this part of subject sequence: showever, with the control in this control is a sequence.
  Scors = 25.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Dius/Flus
Quarry 9 TCARAGCCARACA 16
Sbjek 2989642 TOXAGCOAXACA 2969854
 Peatures in this part of subject sequence: 
lnad discriminguization
  Score = 26.3 bits (13), Espect = 613 Identifies = 13/13 (100%), Gaps = 9/13 (0%) Strand=Phs/Plos
                                             ICANAGCCANACA 16
 Features in this part of subject sequence: cluster():ikVA_reductase
  Scora = 25.3 bits (15), Expect = 612 Identities = 13/13 (100%), Gaps = 0/13 (0%) Strand=Plus/Minus
Query 2 UGDUAAAGGCAAA 14
Features in this part of subject sequence:
  Score = 26.3 bits (53), Expect = -612
Identities = 15/15 (100%), Gaps = 9/13 (0%)
Strand-Flus/Flus
                                          TCARAGCCARACA 16
 > 🗖 <u>gh/AC154968.21</u> 💥 Mus musculus BAC clone RF24-145022 from 14, complete sequence
 Length=149772
  Score = 30.2 bits (15), Expect = 39 Edentities = 15/15 (1008), Gaps = 9/15 (08) Strend-Flus/Flus
                                             TGTCAAAGCCAAACA 16
SECTION OF THE SECTIO
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Get selected sequences Select all Deselect all Distance tree of results

Control (Sections 199 on Laurescent); Control (Sen Section)